



## SEQUENCE LISTING

<110> Freyssinet, Georges  
Rang, Cecile  
Frutos, Roger

<120> Pepsin-sensitive modified Bacillus thuringiensis insecticidal toxin

<130> A35992-PCT-USA-A (072667.0191)

<140> 10/665,460

<141> 2003-09-19

<150> PCT/FR02/00772

<151> 2002-03-04

<150> FR 01/03691

<151> 2001-03-19

<160> 160

<170> PatentIn Ver. 2.1

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<211> 2019

<212> DNA

<213> Bacillus thuringiensis

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<221> CDS

<222> (1)..(2019)

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Cys Gly Cys Pro Ser Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp  
20 25 30

cca aat gca gcg tta caa aat atg aac tat aaa gat tac tta caa atg 144  
Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met  
35 40 45

aca gat gag gac tac act gat tct tat ata aat cct agt tta tct att 192  
Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile  
50 55 60

agt ggt aga gat gca gtt cag act gcg ctt act gtt gtt ggg aga ata 240  
Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly Arg Ile  
65 70 75 80

ctc ggg gct tta ggt gtt ccg ttt tct gga caa ata gtg agt ttt tat 288  
Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr  
85 90 95

caa ttc ctt tta aat aca ctg tgg cca gtt aat gat aca gct ata tgg			336
Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp			
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gaa gct ttc atg cga cag gtg gag gaa ctt gtc aat caa caa ata aca			384
Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr			
115	120	125	
gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta gga gac			432
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Asp			
130	135	140	
tct ttt aat gta tat caa cgt tcc ctt caa aat tgg ttg gct gat cga			480
Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg			
145	150	155	160
aat gat aca cga aat tta agt gtt gtt cgt gct caa ttt ata gct tta			528
Asn Asp Thr Arg Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu			
165	170	175	
gac ctt gat ttt gtt aat gct att cca ttg ttt gca gta aat gga cag			576
Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln			
180	185	190	
cag gtt cca tta ctg tca gta tat gca caa gct gtg aat tta cat ttg			624
Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu His Leu			
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Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Asp Arg			
245	250	255	
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Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln Phe Arg			
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Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr			
275	280	285	
tat gat gta cga ctt tat cca acg gga tca aac cca cag ctt aca cgt			912
Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg			
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gag gta tat aca gat ccg att gta ttt aat cca cca gct aat gtt gga			960
Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Val Gly			
305	310	315	320

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tta aca atc agc agt aat cga ttt cca gtt tca tct aat ttt atg gat Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe Met Asp	355	360	365	1104
tat tgg tca gga cat acg tta cgc cgt agt tat ctg aac gat tca gca Tyr Trp Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp Ser Ala	370	375	380	1152
gta caa gaa gat agt tat ggc cta att aca acc aca aga gca aca att Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Arg Ala Thr Ile	385	390	395	400
aat ccc gga gtt gat gga aca aac cgc ata gag tca acg gca gta gat Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala Val Asp	405	410	415	1248
ttt cgt tct gca ttg ata ggt ata tat ggc gtg aat aga gct tct ttt Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala Ser Phe	420	425	430	1296
gtc cca gga ggc ttg ttt aat ggt acg act tct cct gct aat gga gga Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly	435	440	445	1344
tgt aga gat ctc tat gat aca aat gat gaa tta cca cca gat gaa agt Cys Arg Asp Leu Tyr Asp Thr Asn Asp Glu Leu Pro Pro Asp Glu Ser	450	455	460	1392
acc gga agt tca acc cat aga cta tct cat gtt acc ttt ttt agc ttt Thr Gly Ser Ser Thr His Arg Leu Ser His Val Thr Phe Phe Ser Phe	465	470	475	480
caa act aat cag gct gga tct ata gct aat gca gga agt gta cct act Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr	485	490	495	1488
tat gtt tgg acc cgt cgt gat gtg gac ctt aat aat acg att acc cca Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro	500	505	510	1536
aat aga att aca caa tta cca ttg gta aag gca tct gca cct gtt tcg Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser	515	520	525	1584
ggt act acg gtc tta aaa ggt cca gga ttt aca gga ggg ggt ata ctc Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Ile Leu	530	535	540	1632
cga aga aca act aat ggc aca ttt gga acg tta aga gta acg gtt aat				1680

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Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Val	Arg	Phe	Ala	Ser	Thr	
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gga	aat	ttc	agt	ata	agg	gta	ctc	cgt	gga	ggg	gtt	tct	atc	ggt	gat	1776
Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile	Gly	Asp	
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gtt	aga	tta	ggg	agc	aca	atg	aac	aga	ggg	cag	gaa	cta	act	tac	gaa	1824
Val	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	Tyr	Glu	
						595			600			605				
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Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Val	Asn	Ala	Glu	Gly	
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Val	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Asp	Leu	Glu	Ala	Ala	Lys	Lys	
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gcg																2019
Ala																

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Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met	
							35			40			45			
Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile	
							50			55			60			
Ser	Gly	Arg	Asp	Ala	Val	Gln	Thr	Ala	Leu	Thr	Val	Val	Gly	Arg	Ile	
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Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Val	Ser	Phe	Tyr	

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115                    120                    125

Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Asp  
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Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg  
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Asn Asp Thr Arg Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu  
165                    170                    175

Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln  
180                    185                    190

Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu His Leu  
195                    200                    205

Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr  
210                    215                    220

Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu Thr Ala  
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Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Val Gly  
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Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu  
325                    330                    335

Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Asp Arg Leu Asn Ser  
340                    345                    350

Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe Met Asp  
355                    360                    365

Tyr Trp Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp Ser Ala  
370                    375                    380

Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Thr Arg Ala Thr Ile

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Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly			
435	440	445	
Cys Arg Asp Leu Tyr Asp Thr Asn Asp Glu Leu Pro Pro Asp Glu Ser			
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Thr Gly Ser Ser Thr His Arg Leu Ser His Val Thr Phe Phe Ser Phe			
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Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr			
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Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro			
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Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser			
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Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Ile Leu			
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Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr			
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Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp			
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Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu			
595	600	605	
Ser Phe Phe Thr Arg Glu Phe Thr Thr Gly Pro Phe Asn Pro Pro			
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Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly			
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Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro			
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tgt ggg tgt cca tca gat gac gat gtg agg tat cct ttg gca agt gac 96  
Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp  
20 25 30  
  
cca aat gca gcg tta caa aat atg aac tat aaa gat tac tta caa atg 144  
Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met  
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Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile  
50 55 60  
  
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Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly Arg Ile  
65 70 75 80  
  
ctc ggg gct tta ggt gtt ccg ttt tct gga caa ata gtg agt ttt tat 288  
Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr  
85 90 95  
  
caa ttc ctt tta aat aca ctg tgg cca gtt aat gat aca gct ata tgg 336  
Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp  
100 105 110  
  
gaa gct ttc atg cga cag gtg gag gaa ctt gtc aat caa caa ata aca 384  
Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr  
115 120 125  
  
gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta gga gac 432  
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Asp  
130 135 140  
  
tct ttt aat gta tat caa cgt tcc ctt caa aat tgg ttg gct gat cga 480  
Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg  
145 150 155 160  
  
aat gat aca tta aat tta agt gtt cgt gct caa ttt ata gct tta 528  
Asn Asp Thr Leu Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu  
165 170 175

gac ctt gat ttt gtt aat gct att cca ttg ttt gca gta aat gga cag			576
Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln			
180	185	190	
cag gtt cca tta ctg tca gta tat gca caa gct gtg aat tta cat ttg			624
Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu His Leu			
195	200	205	
tta tta tta aaa gat gca tct ctt ttt gga gaa gga tgg gga ttc aca			672
Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr			
210	215	220	
cag ggg gaa att tcc aca tat tat gac cgt caa ttg gaa cta acc gct			720
Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu Thr Ala			
225	230	235	240
aag tac act aat tac tgt gaa act tgg tat aat aca ggt tta gat cgt			768
Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Asp Arg			
245	250	255	
tta aga gga aca aat act gaa agt tgg tta aga tat cat caa ttc cgt			816
Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln Phe Arg			
260	265	270	
aga gaa atg act tta gtg gta tta gat gtt gtg gcg cta ttt cca tat			864
Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr			
275	280	285	
tat gat gta cga ctt tat cca acg gga tca aac cca cag ctt aca cgt			912
Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg			
290	295	300	
gag gta tat aca gat ccg att gta ttt aat cca cca gct aat gtt gga			960
Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Val Gly			
305	310	315	320
ctt tgc cga cgt tgg ggt act aat ccc tat aat act ttt tct gag ctc			1008
Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu			
325	330	335	
gaa aat gcc ttc att cgc cca cca cat ctt ttt gat agg ctg aat agc			1056
Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Asp Arg Leu Asn Ser			
340	345	350	
tta aca atc agc agt aat cga ttt cca gtt tca tct aat ttt atg gat			1104
Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe Met Asp			
355	360	365	
tat tgg tca gga cat acg tta cgc cgt agt tat ctg aac gat tca gca			1152
Tyr Trp Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp Ser Ala			
370	375	380	
gta caa gaa gat agt tat ggc cta att aca acc aca aga gca aca att			1200
Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Arg Ala Thr Ile			
385	390	395	400

aat ccc gga gtt gat gga aca aac cgc ata gag tca acg gca gta gat			1248
Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala Val Asp			
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Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala Ser Phe			
420	425	430	
gtc cca gga ggc ttg ttt aat ggt acg act tct cct gct aat gga gga			1344
Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly			
435	440	445	
tgt aga gat ctc tat gat aca aat gat gaa tta cca cca gat gaa agt			1392
Cys Arg Asp Leu Tyr Asp Thr Asn Asp Glu Leu Pro Pro Asp Glu Ser			
450	455	460	
acc gga agt tca acc cat aga cta tct cat gtt acc ttt ttt agc ttt			1440
Thr Gly Ser Ser Thr His Arg Leu Ser His Val Thr Phe Phe Ser Phe			
465	470	475	480
caa act aat cag gct gga tct ata gct aat gca gga agt gta cct act			1488
Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr			
485	490	495	
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Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro			
500	505	510	
aat aga att aca caa tta cca ttg gta aag gca tct gca cct gtt tcg			1584
Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser			
515	520	525	
ggc act acg gtc tta aaa ggt cca gga ttt aca gga ggg ggt ata ctc			1632
Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu			
530	535	540	
cga aga aca act aat ggc aca ttt gga acg tta aga gta acg gtt aat			1680
Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn			
545	550	555	560
tca cca tta aca caa caa tat cgc cta aga gtt cgt ttt gcc tca aca			1728
Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr			
565	570	575	
gga aat ttc agt ata agg gta ctc cgt gga ggg gtt tct atc ggt gat			1776
Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp			
580	585	590	
gtt aga tta ggg agc aca atg aac aga ggg cag gaa cta act tac gaa			1824
Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu			
595	600	605	
tcc ttt ttc aca aga gag ttt act act act ggt ccg ttc aat ccg cct			1872
Ser Phe Phe Thr Arg Glu Phe Thr Thr Gly Pro Phe Asn Pro Pro			
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ttt aca ttt aca caa gct caa gag att cta aca gtg aat gca gaa ggt			1920

Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly  
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Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro  
645 650 655

gtg aat ccg gca cga gaa gcg gaa gag gat tta gaa gcg gcg aag aaa 2016  
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gcg 2019  
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<223> Artificial sequence description: Cry9Ca1 Leu-164

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35 40 45

Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile  
50 55 60

Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly Arg Ile  
65 70 75 80

Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr  
85 90 95

Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp  
100 105 110

Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr  
115 120 125

Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Asp  
130 135 140

Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg  
145 150 155 160

Asn Asp Thr Leu Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu  
165 170 175

Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln  
180 185 190

Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu His Leu  
195 200 205

Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr  
210 215 220

Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu Thr Ala  
225 230 235 240

Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Asp Arg  
245 250 255

Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln Phe Arg  
260 265 270

Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr  
275 280 285

Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg  
290 295 300

Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Val Gly  
305 310 315 320

Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu  
325 330 335

Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Asp Arg Leu Asn Ser  
340 345 350

Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe Met Asp  
355 360 365

Tyr Trp Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp Ser Ala  
370 375 380

Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Arg Ala Thr Ile  
385 390 395 400

Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala Val Asp  
405 410 415

Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala Ser Phe  
420 425 430

Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly  
435 440 445

Cys Arg Asp Leu Tyr Asp Thr Asn Asp Glu Leu Pro Pro Asp Glu Ser  
450 455 460

Thr Gly Ser Ser Thr His Arg Leu Ser His Val Thr Phe Phe Ser Phe  
465 470 475 480

Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr  
485 490 495

Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro  
500 505 510

Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser  
515 520 525

Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Ile Leu  
530 535 540

Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn  
545 550 555 560

Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr  
565 570 575

Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp  
580 585 590

Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu  
595 600 605

Ser Phe Phe Thr Arg Glu Phe Thr Thr Gly Pro Phe Asn Pro Pro  
610 615 620

Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly  
625 630 635 640

Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro  
645 650 655

Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys  
660 665 670

Ala

<210> 5  
<211> 2019  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Artificial sequence description: Cry9Cai Phe-164

<220>  
<221> CDS  
<222> (1)..(2019)

<400> 5  
atg aat cga aat aat caa aat gaa tat gaa att att gat gcc ccc cat 48  
Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Pro His  
1 5 10 15

tgt	ggg	tgt	cca	tca	gat	gac	gat	gtg	agg	tat	cct	ttg	gca	agt	gac	96
Cys	Gly	Cys	Pro	Ser	Asp	Asp	Asp	Val	Arg	Tyr	Pro	Leu	Ala	Ser	Asp	
20								25					30			
cca	aat	gca	gcg	tta	caa	aat	atg	aac	tat	aaa	gat	tac	tta	caa	atg	144
Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met	
35								40					45			
aca	gat	gag	gac	tac	act	gat	tct	tat	ata	aat	cct	agt	tta	tct	att	192
Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile	
50							55					60				
agt	ggt	aga	gat	gca	gtt	cag	act	gcg	ctt	act	gtt	ggg	aga	ata	240	
Ser	Gly	Arg	Asp	Ala	Val	Gln	Thr	Ala	Leu	Thr	Val	Val	Gly	Arg	Ile	
65							70				75		80			
ctc	ggg	gct	tta	ggt	gtt	ccg	ttt	tct	gga	caa	ata	gtg	agt	ttt	tat	288
Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Val	Ser	Phe	Tyr	
85							90					95				
caa	ttc	ctt	tta	aat	aca	ctg	tgg	cca	gtt	aat	gat	aca	gct	ata	tgg	336
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp	
100							105					110				
gaa	gct	ttc	atg	cga	cag	gtg	gag	gaa	ctt	gtc	aat	caa	caa	ata	aca	384
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr	
115							120					125				
gaa	ttt	gca	aga	aat	cag	gca	ctt	gca	aga	ttg	caa	gga	tta	gga	gac	432
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Asp	
130							135				140					
tct	ttt	aat	gta	tat	caa	cgt	tcc	ctt	caa	aat	tgg	ttg	gct	gat	cga	480
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg	
145							150				155		160			
aat	gat	aca	ttt	aat	tta	agt	gtt	cgt	gct	caa	ttt	ata	gct	tta		528
Asn	Asp	Thr	Phe	Asn	Leu	Ser	Val	Val	Arg	Ala	Gln	Phe	Ile	Ala	Leu	
165							170				175					
gac	ctt	gat	ttt	gtt	aat	gct	att	cca	ttg	ttt	gca	gta	aat	gga	cag	576
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln	
180							185				190					
cag	gtt	cca	tta	ctg	tca	gta	tat	gca	caa	gct	gtg	aat	tta	cat	ttg	624
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Val	Asn	Leu	His	Leu	
195							200				205					
tta	tta	tta	aaa	gat	gca	tct	ttt	gga	gaa	gga	tgg	gga	ttc	aca	672	
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr	
210							215				220					
cag	ggg	gaa	att	tcc	aca	tat	tat	gac	cgt	caa	ttg	gaa	cta	acc	gct	720
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Asp	Arg	Gln	Leu	Glu	Leu	Thr	Ala	
225							230				235		240			

aag tac act aat tac tgt gaa act tgg tat aat aca ggt tta gat cgt Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Asp Arg 245 250 255	768
tta aga gga aca aat act gaa agt tgg tta aga tat cat caa ttc cgt Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln Phe Arg 260 265 270	816
aga gaa atg act tta gtg gta tta gat gtt gtg gcg cta ttt cca tat Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr 275 280 285	864
tat gat gta cga ctt tat cca acg gga tca aac cca cag ctt aca cgt Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg 290 295 300	912
gag gta tat aca gat ccg att gta ttt aat cca cca gct aat gtt gga Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Val Gly 305 310 315 320	960
ctt tgc cga cgt tgg ggt act aat ccc tat aat act ttt tct gag ctc Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu 325 330 335	1008
gaa aat gcc ttc att cgc cca cca cat ctt ttt gat agg ctg aat agc Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Asp Arg Leu Asn Ser 340 345 350	1056
tta aca atc agc agt aat cga ttt cca gtt tca tct aat ttt atg gat Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe Met Asp 355 360 365	1104
tat tgg tca gga cat acg tta cgc cgt agt tat ctg aac gat tca gca Tyr Trp Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp Ser Ala 370 375 380	1152
gta caa gaa gat agt tat ggc cta att aca acc aca aga gca aca att Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Arg Ala Thr Ile 385 390 395 400	1200
aat ccc gga gtt gat gga aca aac cgc ata gag tca acg gca gta gat Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala Val Asp 405 410 415	1248
ttt cgt tct gca ttg ata ggt ata tat ggc gtg aat aga gct tct ttt Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala Ser Phe 420 425 430	1296
gtc cca gga ggc ttg ttt aat ggt acg act tct cct gct aat gga gga Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly 435 440 445	1344
tgt aga gat ctc tat gat aca aat gat gaa tta cca cca gat gaa agt Cys Arg Asp Leu Tyr Asp Thr Asn Asp Glu Leu Pro Pro Asp Glu Ser 450 455 460	1392
acc gga agt tca acc cat aga cta tct cat gtt acc ttt ttt agc ttt	1440

Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe
465				470					475					480	
caa	act	aat	cag	gct	gga	tct	ata	gct	aat	gca	gga	agt	gta	cct	act
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr
				485					490				495		
tat	gtt	tgg	acc	cgt	cgt	gat	gtg	gac	ctt	aat	aat	acg	att	acc	cca
Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro
				500				505				510			
aat	aga	att	aca	caa	tta	cca	ttg	gta	aag	gca	tct	gca	cct	gtt	tcg
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser
				515				520			525				
ggt	act	acg	gtc	tta	aaa	ggt	cca	gga	ttt	aca	gga	ggg	ggt	ata	ctc
Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu
				530			535			540					
cga	aga	aca	act	aat	ggc	aca	ttt	gga	acg	tta	aga	gta	acg	gtt	aat
Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn
				545			550			555			560		
tca	cca	tta	aca	caa	caa	tat	cgc	cta	aga	gtt	cgt	ttt	gcc	tca	aca
Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Val	Arg	Phe	Ala	Ser	Thr
				565			570			575					
gga	aat	tcc	agt	ata	agg	gta	ctc	cgt	gga	ggg	gtt	tct	atc	ggt	gat
Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile	Gly	Asp
				580			585			590					
gtt	aga	tta	ggg	agc	aca	atg	aac	aga	ggg	cag	gaa	cta	act	tac	gaa
Val	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	Tyr	Glu
				595			600			605					
tcc	ttt	ttc	aca	aga	gag	ttt	act	act	act	ggt	ccg	ttc	aat	ccg	cct
Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro
				610			615			620					
ttt	aca	ttt	aca	caa	gct	caa	gag	att	cta	aca	gtg	aat	gca	gaa	gg
Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Val	Asn	Ala	Glu	Gly
				625			630			635			640		
gtt	agc	acc	gg	tt	gaa	tt									
Val	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Asp	Arg	Ile	Glu	Ile	Val	Pro
				645			650			655					
gtg	aat	ccg	gca	cga	gaa	gcg	gaa	gag	gat	tta	gaa	g	g	g	aa
Val	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Asp	Leu	Glu	Ala	Ala	Lys	Lys
				660			665			670					
gcg															2019
Ala															

<212> PRT  
<213> Artificial sequence

<220>  
<223> Artificial sequence description: Cry9Cal Phe-164

<400> 6

Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Pro His  
1 5 10 15

Cys Gly Cys Pro Ser Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp  
20 25 30

Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met  
35 40 45

Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile  
50 55 60

Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly Arg Ile  
65 70 75 80

Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr  
85 90 95

Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp  
100 105 110

Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr  
115 120 125

Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Asp  
130 135 140

Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg  
145 150 155 160

Asn Asp Thr Phe Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu  
165 170 175

Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln  
180 185 190

Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu His Leu  
195 200 205

Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr  
210 215 220

Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu Thr Ala  
225 230 235 240

Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Asp Arg  
245 250 255

Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln Phe Arg  
260 265 270

Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr  
275 280 285

Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg  
290 295 300

Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Val Gly  
305 310 315 320

Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu  
325 330 335

Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Asp Arg Leu Asn Ser  
340 345 350

Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe Met Asp  
355 360 365

Tyr Trp Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp Ser Ala  
370 375 380

Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Arg Ala Thr Ile  
385 390 395 400

Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala Val Asp  
405 410 415

Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala Ser Phe  
420 425 430

Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly  
435 440 445

Cys Arg Asp Leu Tyr Asp Thr Asn Asp Glu Leu Pro Pro Asp Glu Ser  
450 455 460

Thr Gly Ser Ser Thr His Arg Leu Ser His Val Thr Phe Phe Ser Phe  
465 470 475 480

Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr  
485 490 495

Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro  
500 505 510

Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser  
515 520 525

Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu  
530 535 540

Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn  
545 550 555 560

Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr  
565 570 575

Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp  
580 585 590

Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu  
595 600 605

Ser Phe Phe Thr Arg Glu Phe Thr Thr Gly Pro Phe Asn Pro Pro  
610 615 620

Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly  
625 630 635 640

Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro  
645 650 655

Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys  
660 665 670

Ala

<210> 7

<211> 2019

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: Cry9Ca1 Glu-164

<220>

<221> CDS

<222> (1)..(2019)

<400> 7

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Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Pro His  
1 5 10 15

tgt ggg tgt cca tca gat gac gat gtg agg tat cct ttg gca agt gac 96  
Cys Gly Cys Pro Ser Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp  
20 25 30

cca aat gca gcg tta caa aat atg aac tat aaa gat tac tta caa atg 144  
Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met  
35 40 45

aca gat gag gac tac act gat tct tat ata aat cct agt tta tct att 192  
Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile  
50 55 60

agt ggt aga gat gca gtt cag act gcg ctt act gtt gtt ggg aga ata 240  
Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly Arg Ile  
65 70 75 80

ctc ggg gct tta ggt gtt ccg ttt tct gga caa ata gtg agt ttt tat		288	
Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr			
85	90	95	
caa ttc ctt tta aat aca ctg tgg cca gtt aat gat aca gct ata tgg		336	
Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp			
100	105	110	
gaa gct ttc atg cga cag gtg gag gaa ctt gtc aat caa caa ata aca		384	
Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr			
115	120	125	
gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta gga gac		432	
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Asp			
130	135	140	
tct ttt aat gta tat caa cgt tcc ctt caa aat tgg ttg gct gat cga		480	
Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg			
145	150	155	160
aat gat aca gaa aat tta agt gtt gtt cgt gct caa ttt ata gct tta		528	
Asn Asp Thr Glu Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu			
165	170	175	
gac ctt gat ttt gtt aat gct att cca ttg ttt gca gta aat gga cag		576	
Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln			
180	185	190	
cag gtt cca tta ctg tca gta tat gca caa gct gtg aat tta cat ttg		624	
Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu His Leu			
195	200	205	
tta tta tta aaa gat gca tct ctt ttt gga gaa gga tgg gga ttc aca		672	
Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr			
210	215	220	
cag ggg gaa att tcc aca tat tat gac cgt caa ttg gaa cta acc gct		720	
Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu Thr Ala			
225	230	235	240
aag tac act aat tac tgt gaa act tgg tat aat aca ggt tta gat cgt		768	
Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Asp Arg			
245	250	255	
tta aga gga aca aat act gaa agt tgg tta aga tat cat caa ttc cgt		816	
Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln Phe Arg			
260	265	270	
aga gaa atg act tta gtg gta tta gat gtt gtg gcg cta ttt cca tat		864	
Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr			
275	280	285	
tat gat gta cga ctt tat cca acg gga tca aac cca cag ctt aca cgt		912	
Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg			
290	295	300	
gag gta tat aca gat ccg att gta ttt aat cca cca gct aat gtt gga		960	

Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Val	Gly	
305																320
ctt	tgc	cga	cgt	tgg	ggt	act	aat	ccc	tat	aat	act	ttt	tct	gag	ctc	1008
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu	
																325
325																335
330																
gaa	aat	gcc	ttc	att	cgc	cca	cca	cat	ctt	ttt	gat	agg	ctg	aat	agc	1056
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser	
																340
340																345
345																350
tta	aca	atc	agc	agt	aat	cga	ttt	cca	gtt	tca	tct	aat	ttt	atg	gat	1104
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp	
																355
355																360
360																365
365																
tat	tgg	tca	gga	cat	acg	tta	cgc	cgt	agt	tat	ctg	aac	gat	tca	gca	1152
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala	
																370
370																375
375																380
380																
gta	caa	gaa	gat	agt	tat	ggc	cta	att	aca	acc	aca	aga	gca	aca	att	1200
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile	
																385
385																390
390																395
395																400
400																
aat	ccc	gga	gtt	gat	gga	aca	aac	cgc	ata	gag	tca	acg	gca	gta	gat	1248
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp	
																405
405																410
410																415
415																
ttt	cgt	tct	gca	ttg	ata	ggt	ata	tat	ggc	gtg	aat	aga	gct	tct	ttt	1296
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe	
																420
420																425
425																430
430																
gtc	cca	gga	ggc	ttg	ttt	aat	ggt	acg	act	tct	cct	gct	aat	gga	gga	1344
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly	
																435
435																440
440																445
445																
tgt	aga	gat	ctc	tat	gat	aca	aat	gat	gaa	tta	cca	cca	gat	gaa	agt	1392
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser	
																450
450																455
455																460
460																
acc	gga	agt	tca	acc	cat	aga	cta	tct	cat	gtt	acc	ttt	ttt	agc	ttt	1440
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe	
																465
465																470
470																475
475																480
480																
caa	act	aat	cag	gct	gga	tct	ata	gct	aat	gca	gga	agt	gta	cct	act	1488
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr	
																485
485																490
490																495
495																
tat	gtt	tgg	acc	cgt	cgt	gat	gtg	gac	ctt	aat	aat	acg	att	acc	cca	1536
Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro	
																500
500																505
505																510
510																
aat	aga	att	aca	caa	tta	cca	ttg	gta	aag	gca	tct	gca	cct	gtt	tcg	1584
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser	
																515
515																520
520																525
525																
ggt	act	acg	gtc	tta	aaa	ggt	cca	gga	ttt	aca	gga	ggg	ggt	ata	ctc	1632
Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Ile	Leu		

530	535	540	
cga aga aca act aat ggc aca ttt gga acg tta aga gta acg gtt aat			1680
Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn			
545	550	555	560
tca cca tta aca caa caa tat cgc cta aga gtt cgt ttt gcc tca aca			1728
Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr			
565	570	575	
gga aat ttc agt ata agg gta ctc cgt gga ggg gtt tct atc ggt gat			1776
Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp			
580	585	590	
gtt aga tta ggg agc aca atg aac aga ggg cag gaa cta act tac gaa			1824
Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu			
595	600	605	
tcc ttt ttc aca aga gag ttt act act act ggt ccg ttc aat ccg cct			1872
Ser Phe Phe Thr Arg Glu Phe Thr Thr Gly Pro Phe Asn Pro Pro			
610	615	620	
ttt aca ttt aca caa gct caa gag att cta aca gtg aat gca gaa ggt			1920
Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly			
625	630	635	640
gtt agc acc ggt ggt gaa tat tat ata gat aga att gaa att gtc cct			1968
Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro			
645	650	655	
gtg aat ccg gca cga gaa gcg gaa gag gat tta gaa gcg gcg aag aaa			2016
Val Asn Pro Ala Arg Glu Ala Glu Asp Leu Glu Ala Ala Lys Lys			
660	665	670	
gcg			2019
Ala			

<210> 8  
<211> 673  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Artificial sequence description: Cry9Cai Glu-164

<400> 8  
Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Pro His  
1 5 10 15

Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp  
20 25 30

Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met  
35 40 45

Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile

50	55	60													
Ser	Gly	Arg	Asp	Ala	Val	Gln	Thr	Ala	Leu	Thr	Val	Val	Gly	Arg	Ile
65					70					75					80
Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Val	Ser	Phe	Tyr
					85				90						95
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp
					100				105						110
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr
					115			120							125
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Asp
					130			135							140
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg
145					150				155						160
Asn	Asp	Thr	Glu	Asn	Leu	Ser	Val	Val	Arg	Ala	Gln	Phe	Ile	Ala	Leu
					165			170							175
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln
					180			185							190
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Val	Asn	Leu	His	Leu
					195			200							205
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr
					210			215							220
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Asp	Arg	Gln	Leu	Glu	Leu	Thr	Ala
225					230				235						240
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Asp	Arg
					245			250							255
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Trp	Leu	Arg	Tyr	His	Gln	Phe	Arg
					260			265							270
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr
					275			280							285
Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg
					290			295							300
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Val	Gly
					305			310			315				320
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu
					325			330							335
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser
					340			345							350
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp

355                    360                    365

Tyr Trp Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp Ser Ala  
370                    375                    380

Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Thr Arg Ala Thr Ile  
385                    390                    395                    400

Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala Val Asp  
405                    410                    415

Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala Ser Phe  
420                    425                    430

Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly  
435                    440                    445

Cys Arg Asp Leu Tyr Asp Thr Asn Asp Glu Leu Pro Pro Asp Glu Ser  
450                    455                    460

Thr Gly Ser Ser Thr His Arg Leu Ser His Val Thr Phe Phe Ser Phe  
465                    470                    475                    480

Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr  
485                    490                    495

Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro  
500                    505                    510

Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser  
515                    520                    525

Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Ile Leu  
530                    535                    540

Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn  
545                    550                    555                    560

Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr  
565                    570                    575

Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp  
580                    585                    590

Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu  
595                    600                    605

Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro  
610                    615                    620

Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly  
625                    630                    635                    640

Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro  
645                    650                    655

Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys

660

665

670

Ala

<210> 9

<211> 2019

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: Cry9Ca1-100%

<220>

<221> CDS

<222> (1)..(2019)

<400> 9

atg aat cga aat aat caa aat gaa tat gaa att att gaa gcc ccc cat 48  
Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Glu Ala Pro His  
1 5 10 15

tgt ggg tgt cca tca gaa gaa gaa tta agg tat cct ttg gca agt gaa 96  
Cys Gly Cys Pro Ser Glu Glu Leu Arg Tyr Pro Leu Ala Ser Glu  
20 25 30

cca aat gca gcg tta caa aat atg aac tat aaa gaa tac tta caa atg 144  
Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Glu Tyr Leu Gln Met  
35 40 45

aca gaa gag gaa tac act gaa tct tat ata aat cct agt tta tct att 192  
Thr Glu Glu Glu Tyr Thr Glu Ser Tyr Ile Asn Pro Ser Leu Ser Ile  
50 55 60

agt ggt aga gaa gca tta cag act gcg ctt act gtt att agg aga ata 240  
Ser Gly Arg Glu Ala Leu Gln Thr Ala Leu Thr Val Ile Arg Arg Ile  
65 70 75 80

ctc ggg gct tta ggt tta ccg ttt tct gga caa ata tta agt ttt tat 288  
Leu Gly Ala Leu Gly Leu Pro Phe Ser Gly Gln Ile Leu Ser Phe Tyr  
85 90 95

caa ttc ctt tta aat aca ctg ttt cca tta aat gaa aca gct ata ttt 336  
Gln Phe Leu Leu Asn Thr Leu Phe Pro Leu Asn Glu Thr Ala Ile Phe  
100 105 110

gaa gct ttc atg cga cag tta gag gaa ctt tta aat caa caa ata aca 384  
Glu Ala Phe Met Arg Gln Leu Glu Glu Leu Leu Asn Gln Gln Ile Thr  
115 120 125

gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta gga gaa 432  
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Glu  
130 135 140

tct ttt aat tta tat caa cgt tcc ctt caa aat ttt ttg gct gaa cga 480

Ser	Phe	Asn	Leu	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Phe	Leu	Ala	Glu	Arg	
145				150					155				160			
aat	gaa	aca	cga	aat	tta	agt	tta	tta	cgt	gct	caa	ttt	ata	gct	tta	528
Asn	Glu	Thr	Arg	Asn	Leu	Ser	Leu	Leu	Arg	Ala	Gln	Phe	Ile	Ala	Leu	
				165					170				175			
gaa	ctt	gaa	ttt	tta	aat	gct	att	cca	ttg	ttt	gca	tta	aat	gga	cag	576
Glu	Leu	Glu	Phe	Leu	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Leu	Asn	Gly	Gln	
				180				185				190				
cag	tta	cca	tta	ctg	tca	tta	tat	gca	caa	gct	tta	aat	tta	cat	ttg	624
Gln	Leu	Pro	Leu	Leu	Ser	Leu	Tyr	Ala	Gln	Ala	Leu	Asn	Leu	His	Leu	
				195				200				205				
tta	tta	tta	aaa	gaa	gca	tct	ctt	ttt	gga	gaa	gga	ttt	gga	ttc	aca	672
Leu	Leu	Leu	Lys	Glu	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Phe	Gly	Phe	Thr	
				210				215				220				
cag	ggg	gaa	att	tcc	aca	tat	tat	gaa	cgt	caa	ttg	gaa	cta	acc	gct	720
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Glu	Arg	Gln	Leu	Glu	Leu	Thr	Ala	
				225				230			235		240			
aag	tac	act	aat	tac	tgt	gaa	act	ttt	tat	aat	aca	ggt	tta	gaa	cgt	768
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Phe	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	
				245				250				255				
tta	aga	gga	aca	aat	act	gaa	agt	ttt	tta	aga	tat	cat	caa	ttc	cgt	816
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Phe	Leu	Arg	Tyr	His	Gln	Phe	Arg	
				260				265				270				
aga	gaa	atg	act	tta	tta	tta	tta	gaa	tta	tta	gcg	cta	ttt	cca	tat	864
Arg	Glu	Met	Thr	Leu	Leu	Leu	Leu	Glu	Leu	Leu	Ala	Leu	Phe	Pro	Tyr	
				275				280				285				
tat	gaa	tta	cga	ctt	tat	cca	acg	gga	tca	aac	cca	cag	ctt	aca	cgt	912
Tyr	Glu	Leu	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg	
				290				295				300				
gag	tta	tat	aca	gaa	ccg	att	tta	ttt	aat	cca	cca	gct	aat	tta	gga	960
Glu	Leu	Tyr	Thr	Glu	Pro	Ile	Leu	Phe	Asn	Pro	Pro	Ala	Asn	Leu	Gly	
				305				310			315		320			
ctt	tgc	cga	cgt	ttt	ggt	act	aat	ccc	tat	aat	act	ttt	tct	gag	ctc	1008
Leu	Cys	Arg	Arg	Phe	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu	
				325				330				335				
gaa	aat	gcc	ttc	att	cgc	cca	cca	cat	ctt	ttt	gaa	agg	ctg	aat	agc	1056
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Glu	Arg	Leu	Asn	Ser	
				340				345				350				
tta	aca	atc	agc	agt	aat	cga	ttt	cca	tta	tca	tct	aat	ttt	atg	gaa	1104
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Leu	Ser	Ser	Asn	Phe	Met	Glu	
				355				360				365				
tat	ttt	tca	gga	cat	acg	tta	cgc	cgt	agt	tat	ctg	aac	gaa	tca	gca	1152
Tyr	Phe	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Glu	Ser	Ala	

370	375	380	
tta caa gaa gaa agt tat ggc cta att aca acc aca aca gca aca att Leu Gln Glu Glu Ser Tyr Gly Leu Ile Thr Thr Thr Arg Ala Thr Ile 385	390	395	1200
aat ccc gga tta gaa gga aca aac cgc ata gag tca acg gca tta gaa Asn Pro Gly Leu Glu Gly Thr Asn Arg Ile Glu Ser Thr Ala Leu Glu 405	410	415	1248
ttt cgt tct gca ttg ata ggt ata tat ggc tta aat aga gct tct ttt Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Leu Asn Arg Ala Ser Phe 420	425	430	1296
tta cca gga ggc ttg ttt aat ggt acg act tct cct gct aat gga gga Leu Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly 435	440	445	1344
tgt aga gaa ctc tat gaa aca aat gaa gaa tta cca cca gaa gaa agt Cys Arg Glu Leu Tyr Glu Thr Asn Glu Glu Leu Pro Pro Glu Glu Ser 450	455	460	1392
acc gga agt tca acc cat aga cta tct cat tta acc ttt ttt agc ttt Thr Gly Ser Ser Thr His Arg Leu Ser His Leu Thr Phe Phe Ser Phe 465	470	475	1440
caa act aat cag gct gga tct ata gct aat gca gga agt tta cct act Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Leu Pro Thr 485	490	495	1488
tat tta ttt acc cgt cgt gaa tta gaa ctt aat aat acg att acc cca Tyr Leu Phe Thr Arg Arg Glu Leu Glu Leu Asn Asn Thr Ile Thr Pro 500	505	510	1536
aat aga att aca caa tta cca ttg tta aag gca tct gca cct tta tcg Asn Arg Ile Thr Gln Leu Pro Leu Leu Lys Ala Ser Ala Pro Leu Ser 515	520	525	1584
ggg act acg tta tta aaa ggt cca gga ttt aca gga ggg ggt ata ctc Gly Thr Thr Leu Leu Lys Gly Pro Gly Phe Thr Gly Gly Ile Leu 530	535	540	1632
cga aga aca act aat ggc aca ttt gga acg tta aga tta acg tta aat Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Leu Thr Leu Asn 545	550	555	1680
tca cca tta aca caa caa tat cgc cta aga tta cgt ttt gcc tca aca Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Leu Arg Phe Ala Ser Thr 565	570	575	1728
gga aat ttc agt ata agg tta ctc cgt gga ggg tta tct atc ggt gaa Gly Asn Phe Ser Ile Arg Leu Leu Arg Gly Gly Leu Ser Ile Gly Glu 580	585	590	1776
tta aga tta ggg agc aca atg aac aga ggg cag gaa cta act tac gaa Leu Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu 595	600	605	1824

tcc ttt ttc aca aga gag ttt act act act ggt ccg ttc aat ccg cct	1872
Ser Phe Phe Thr Arg Glu Phe Thr Thr Gly Pro Phe Asn Pro Pro	
610 615 620	
ttt aca ttt aca caa gct caa gag att cta aca tta aat gca gaa ggt	1920
Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Leu Asn Ala Glu Gly	
625 630 635 640	
tta agc acc ggt ggt gaa tat tat ata gaa aga att gaa att tta cct	1968
Leu Ser Thr Gly Gly Glu Tyr Tyr Ile Glu Arg Ile Glu Ile Leu Pro	
645 650 655	
tta aat ccg gca cga gaa gcg gaa gag gaa tta gaa gcg gcg aag aaa	2016
Leu Asn Pro Ala Arg Glu Ala Glu Glu Leu Glu Ala Ala Lys Lys	
660 665 670	
gcg	2019
Ala	

<210> 10  
<211> 673  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Artificial sequence description: Cry9Ca1-100%

<400> 10  
Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Glu Ala Pro His  
1 5 10 15

Cys Gly Cys Pro Ser Glu Glu Leu Arg Tyr Pro Leu Ala Ser Glu  
20 25 30

Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Glu Tyr Leu Gln Met  
35 40 45

Thr Glu Glu Glu Tyr Thr Glu Ser Tyr Ile Asn Pro Ser Leu Ser Ile  
50 55 60

Ser Gly Arg Glu Ala Leu Gln Thr Ala Leu Thr Val Ile Arg Arg Ile  
65 70 75 80

Leu Gly Ala Leu Gly Leu Pro Phe Ser Gly Gln Ile Leu Ser Phe Tyr  
85 90 95

Gln Phe Leu Leu Asn Thr Leu Phe Pro Leu Asn Glu Thr Ala Ile Phe  
100 105 110

Glu Ala Phe Met Arg Gln Leu Glu Glu Leu Leu Asn Gln Gln Ile Thr  
115 120 125

Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Glu  
130 135 140

Ser Phe Asn Leu Tyr Gln Arg Ser Leu Gln Asn Phe Leu Ala Glu Arg  
145 150 155 160

Asn Glu Thr Arg Asn Leu Ser Leu Leu Arg Ala Gln Phe Ile Ala Leu  
165 170 175

Glu Leu Glu Phe Leu Asn Ala Ile Pro Leu Phe Ala Leu Asn Gly Gln  
180 185 190

Gln Leu Pro Leu Leu Ser Leu Tyr Ala Gln Ala Leu Asn Leu His Leu  
195 200 205

Leu Leu Leu Lys Glu Ala Ser Leu Phe Gly Glu Gly Phe Gly Phe Thr  
210 215 220

Gln Gly Glu Ile Ser Thr Tyr Tyr Glu Arg Gln Leu Glu Leu Thr Ala  
225 230 235 240

Lys Tyr Thr Asn Tyr Cys Glu Thr Phe Tyr Asn Thr Gly Leu Glu Arg  
245 250 255

Leu Arg Gly Thr Asn Thr Glu Ser Phe Leu Arg Tyr His Gln Phe Arg  
260 265 270

Arg Glu Met Thr Leu Leu Leu Leu Glu Leu Leu Ala Leu Phe Pro Tyr  
275 280 285

Tyr Glu Leu Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg  
290 295 300

Glu Leu Tyr Thr Glu Pro Ile Leu Phe Asn Pro Pro Ala Asn Leu Gly  
305 310 315 320

Leu Cys Arg Arg Phe Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu  
325 330 335

Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Glu Arg Leu Asn Ser  
340 345 350

Leu Thr Ile Ser Ser Asn Arg Phe Pro Leu Ser Ser Asn Phe Met Glu  
355 360 365

Tyr Phe Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Glu Ser Ala  
370 375 380

Leu Gln Glu Glu Ser Tyr Gly Leu Ile Thr Thr Thr Arg Ala Thr Ile  
385 390 395 400

Asn Pro Gly Leu Glu Gly Thr Asn Arg Ile Glu Ser Thr Ala Leu Glu  
405 410 415

Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Leu Asn Arg Ala Ser Phe  
420 425 430

Leu Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly  
435 440 445

Cys Arg Glu Leu Tyr Glu Thr Asn Glu Glu Leu Pro Pro Glu Glu Ser  
450 455 460

Thr Gly Ser Ser Thr His Arg Leu Ser His Leu Thr Phe Phe Ser Phe  
465 470 475 480

Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Leu Pro Thr  
485 490 495

Tyr Leu Phe Thr Arg Arg Glu Leu Glu Leu Asn Asn Thr Ile Thr Pro  
500 505 510

Asn Arg Ile Thr Gln Leu Pro Leu Leu Lys Ala Ser Ala Pro Leu Ser  
515 520 525

Gly Thr Thr Leu Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu  
530 535 540

Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Leu Thr Leu Asn  
545 550 555 560

Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Leu Arg Phe Ala Ser Thr  
565 570 575

Gly Asn Phe Ser Ile Arg Leu Leu Arg Gly Gly Leu Ser Ile Gly Glu  
580 585 590

Leu Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu  
595 600 605

Ser Phe Phe Thr Arg Glu Phe Thr Thr Gly Pro Phe Asn Pro Pro  
610 615 620

Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Leu Asn Ala Glu Gly  
625 630 635 640

Leu Ser Thr Gly Gly Glu Tyr Tyr Ile Glu Arg Ile Glu Ile Leu Pro  
645 650 655

Leu Asn Pro Ala Arg Glu Ala Glu Glu Leu Glu Ala Ala Lys Lys  
660 665 670

Ala

<210> 11  
<211> 2019  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Artificial sequence description: Cry9Ca1-25%

<220>  
<221> CDS

<222> (1)..(2019)

<400> 11  
atg aat cga aat aat caa aat gaa tat gaa att att gat gcc ccc cat 48  
Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Pro His  
1 5 10 15  
  
tgt ggg tgt cca tca gat gac gat gtg agg tat cct ttg gca agt gac 96  
Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp  
20 25 30  
  
cca aat gca gcg tta caa aat atg aac tat aaa gat tac tta caa atg 144  
Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met  
35 40 45  
  
aca gat gag gac tac act gat tct tat ata aat cct agt tta tct att 192  
Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile  
50 55 60  
  
agt ggt aga gaa gca tta cag act gcg ctt acg tta tta ggg aga ata 240  
Ser Gly Arg Glu Ala Leu Gln Thr Ala Leu Thr Leu Leu Gly Arg Ile  
65 70 75 80  
  
ctc ggg gct tta ggt gtt ccg ttt tct gga caa ata tta agt ttt tat 288  
Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Leu Ser Phe Tyr  
85 90 95  
  
caa ttc ctt tta aat aca ctg tgg cca gtt aat gat aca gct ata tgg 336  
Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp  
100 105 110  
  
gaa gct ttc atg cga cag gtg gag gaa ctt gtc aat caa caa ata aca 384  
Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr  
115 120 125  
  
gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta gga gaa 432  
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Glu  
130 135 140  
  
tct ttt aat gta tat caa cgt tcc ctt caa aat tgg ttg gct gat cga 480  
Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg  
145 150 155 160  
  
aat gat aca cga aat tta agt tta cgt gct caa ttt ata gct tta 528  
Asn Asp Thr Arg Asn Leu Ser Leu Leu Arg Ala Gln Phe Ile Ala Leu  
165 170 175  
  
gac ctt gat ttt gtt aat gct att cca ttg ttt gca gta aat gga cag 576  
Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln  
180 185 190  
  
cag gtt cca tta ctg tca gta tat gca caa gct tta aat tta cat ttg 624  
Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Leu Asn Leu His Leu  
195 200 205  
  
tta tta tta aaa gaa gca tct ctt ttt gga gaa gga tgg gga ttc aca 672  
Leu Leu Leu Lys Glu Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr

210	215	220	
cag ggg gaa att tcc aca tat tat gaa cgt caa ttg gaa cta acc gct Gln Gly Glu Ile Ser Thr Tyr Tyr Glu Arg Gln Leu Glu Leu Thr Ala 225	230	235	720
aag tac act aat tac tgt gaa act tgg tat aat aca ggt tta gaa cgt Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Glu Arg 245	250	255	768
tta aga gga aca aat act gaa agt ttt tta aga tat cat caa ttc cgt Leu Arg Gly Thr Asn Thr Glu Ser Phe Leu Arg Tyr His Gln Phe Arg 260	265	270	816
aga gaa atg act tta gtg gta tta gat gtt gtg gcg cta ttt cca tat Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr 275	280	285	864
tat gat gta cga ctt tat cca acg gga tca aac cca cag ctt aca cgt Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg 290	295	300	912
gag gta tat aca gat ccg att gta ttt aat cca cca gct aat tta gga Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Leu Gly 305	310	315	960
ctt tgc cga cgt tgg ggt act aat ccc tat aat act ttt tct gag ctc Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu 325	330	335	1008
gaa aat gcc ttc att cgc cca cca cat ctt ttt gaa agg ctg aat agc Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Glu Arg Leu Asn Ser 340	345	350	1056
tta aca atc agc agt aat cga ttt cca gtt tca tct aat ttt atg gaa Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe Met Glu 355	360	365	1104
tat ttt tca gga cat acg tta cgc cgt agt tat ctg aac gat tca gca Tyr Phe Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp Ser Ala 370	375	380	1152
gta caa gaa gat agt tat ggc cta att aca acc aca aga gca aca att Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Arg Ala Thr Ile 385	390	395	1200
aat ccc gga gtt gat gga aca aac cgc ata gag tca acg gca gta gat Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala Val Asp 405	410	415	1248
ttt cgt tct gca ttg ata ggt ata tat ggc gtg aat aga gct tct ttt Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala Ser Phe 420	425	430	1296
gtc cca gga ggc ttg ttt aat ggt acg act tct cct gct aat gga gga Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly 435	440	445	1344

tgt	aga	gat	ctc	tat	gat	aca	aat	gat	gaa	tta	cca	cca	gat	gaa	agt	1392	
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser		
450						455					460						
acc	gga	agt	tca	acc	cat	aga	cta	tct	cat	tta	acc	ttt	ttt	agc	ttt	1440	
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Leu	Thr	Phe	Phe	Ser	Phe		
465							470				475			480			
caa	act	aat	cag	gct	gga	tct	ata	gct	aat	gca	gga	agt	gta	cct	act	1488	
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr		
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tat	gtt	tgg	acc	cgt	cgt	gat	gtg	gac	ctt	aat	aat	acg	att	acc	cca	1536	
Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro		
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aat	aga	att	aca	caa	tta	cca	ttg	gta	aag	gca	tct	gca	cct	gtt	tcg	1584	
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ggg	act	acg	gtc	tta	aaa	ggg	cca	gga	ttt	aca	gga	ggg	ggg	ggg	ata	ctc	1632
Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu		
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cga	aga	aca	act	aat	ggc	aca	ttt	gga	acg	tta	aga	gta	acg	gtt	aat	1680	
Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn		
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tca	cca	tta	aca	caa	caa	tat	cgc	cta	aga	tta	cgt	ttt	gcc	tca	aca	1728	
Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Leu	Arg	Phe	Ala	Ser	Thr		
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gga	aat	tcc	agt	ata	agg	gta	ctc	cgt	gga	ggg	gtt	tct	atc	ggg	gat	1776	
Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile	Gly	Asp		
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gtt	aga	tta	ggg	agc	aca	atg	aac	aga	ggg	cag	gaa	cta	act	tac	gaa	1824	
Val	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	Tyr	Glu		
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tcc	ttt	tcc	aca	aga	gag	ttt	act	act	act	ggt	ccg	ttc	aat	ccg	cct	1872	
Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro		
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ttt	aca	ttt	aca	caa	gct	caa	gag	att	cta	aca	gtg	aat	gca	gaa	ggg	1920	
Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Val	Asn	Ala	Glu	Gly		
							625			630			635		640		
gtt	agc	acc	ggg	ggt	gaa	tat	tat	ata	gat	aga	att	gaa	att	gtc	cct	1968	
Val	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Asp	Arg	Ile	Glu	Ile	Val	Pro		
							645			650			655				
gtg	aat	ccg	gca	cga	gaa	gcg	gaa	gag	gat	tta	gaa	gcg	gcg	aag	aaa	2016	
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gcf  
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2019

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Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met  
35 40 45  
  
Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile  
50 55 60  
  
Ser Gly Arg Glu Ala Leu Gln Thr Ala Leu Thr Leu Leu Gly Arg Ile  
65 70 75 80  
  
Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Leu Ser Phe Tyr  
85 90 95  
  
Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp  
100 105 110  
  
Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr  
115 120 125  
  
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Glu  
130 135 140  
  
Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg  
145 150 155 160  
  
Asn Asp Thr Arg Asn Leu Ser Leu Leu Arg Ala Gln Phe Ile Ala Leu  
165 170 175  
  
Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln  
180 185 190  
  
Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Leu Asn Leu His Leu  
195 200 205  
  
Leu Leu Leu Lys Glu Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr  
210 215 220  
  
Gln Gly Glu Ile Ser Thr Tyr Tyr Glu Arg Gln Leu Glu Leu Thr Ala  
225 230 235 240

Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Glu Arg  
245 250 255

Leu Arg Gly Thr Asn Thr Glu Ser Phe Leu Arg Tyr His Gln Phe Arg  
260 265 270

Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr  
275 280 285

Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg  
290 295 300

Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Leu Gly  
305 310 315 320

Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu  
325 330 335

Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Glu Arg Leu Asn Ser  
340 345 350

Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe Met Glu  
355 360 365

Tyr Phe Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp Ser Ala  
370 375 380

Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Arg Ala Thr Ile  
385 390 395 400

Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala Val Asp  
405 410 415

Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala Ser Phe  
420 425 430

Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly  
435 440 445

Cys Arg Asp Leu Tyr Asp Thr Asn Asp Glu Leu Pro Pro Asp Glu Ser  
450 455 460

Thr Gly Ser Ser Thr His Arg Leu Ser His Leu Thr Phe Phe Ser Phe  
465 470 475 480

Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr  
485 490 495

Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro  
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Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser  
515 520 525

Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu  
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Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn  
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Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Leu Arg Phe Ala Ser Thr  
565 570 575  
Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp  
580 585 590  
Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu  
595 600 605  
Ser Phe Phe Thr Arg Glu Phe Thr Thr Gly Pro Phe Asn Pro Pro  
610 615 620  
Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly  
625 630 635 640  
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<223> Artificial sequence description: mutant 3

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<223> Artificial sequence description: mutant 4

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<223> Artificial sequence description: mutant 5

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<210> 18  
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<223> Artificial sequence description: mutant 6

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<210> 19  
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<223> Artificial sequence description: mutant 7

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<210> 21  
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gaattattag aagaagaaga attaagtgtt 30

<210> 22  
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<223> Artificial sequence description: mutant 22

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<210> 35  
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<223> Artificial sequence description: mutant 23

<400> 35  
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<223> Artificial sequence description: mutant 24

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ttagaattat taaat 15

<210> 37  
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<223> Artificial sequence description: mutant 25

<400> 37  
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<210> 38  
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<223> Artificial sequence description: mutant 26

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<210> 39  
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<210> 40  
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<210> 41  
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<210> 42  
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<210> 45  
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<210> 46  
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<210> 49
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<210> 67  
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<210> 68  
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<400> 68  
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<210> 69  
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<210> 78  
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<210> 79  
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<400> 79  
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<210> 80  
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<210> 81  
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oligonucleotide 40

<400> 81  
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<210> 82  
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<210> 83

<211> 45  
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<400> 83  
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<210> 84  
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<400> 84  
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<210> 85  
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oligonucleotide 44

<400> 85  
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<210> 86  
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<210> 87  
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<210> 88  
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<210> 89  
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<400> 89  
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<210> 90  
<211> 39  
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<210> 91  
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<210> 92  
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<210> 93  
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<210> 94  
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oligonucleotide 53

<400> 94  
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<210> 95  
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oligonucleotide 54

<400> 95  
tgggtgtcca tcagaagaag aattaaggta tcctttggca 40

<210> 96  
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<400> 96  
tcctttggca agtgaaccaa atgcagc 27

<210> 97  
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oligonucleotide 56

<400> 97  
gaactataaa gaatacttac aaatg 25

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caaatgacag aagaggaata cactga 26

<210> 99  
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<220>

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oligonucleotide 58

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tacactgaat ctttatataaa 20

<210> 100  
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<210> 101  
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oligonucleotide 60

<400> 101  
cagactgcgc ttactgttat tagggagaat actcgaa 37

<210> 102  
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oligonucleotide 61

<400> 102  
gggctttagg tttaccgttt tctgg 25

<210> 103  
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oligonucleotide 62

<400> 103  
ttctggacaa atattaagtt tttatcaa 28

<210> 104  
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oligonucleotide 63

<400> 104  
cttttaaata cactgttcc attaaatgaa acagctatat 40

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<210> 106  
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cttccatgcg acagtttagag gaactt 26

<210> 107  
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gaggaacttt taaatcaaca aataac 26

<210> 108  
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<210> 109  
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<210> 110
<211> 21
<212> DNA
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      oligonucleotide 69

<400> 110
ccttcaaaaat tttttggctg a

<210> 111
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<400> 111
ttggctgaac gaaatga

<210> 112
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cgaaatgaaa cacgaaaattt aag

<210> 113
<211> 37
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<220>
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acacgaaatt taagtttatt acgtgctcaa tttatag

37

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48

<210> 115  
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27

<210> 116  
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27

<210> 117  
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<400> 117  
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27

<210> 118  
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tatgcacaag ctttaaattt acatttg 27

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<210> 120  
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tggagaagga tttggattca cacag 25

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<210> 122  
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oligonucleotide 81

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tactgtgaaa cttttataa tacaggtt 28

<210> 123  
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oligonucleotide 82

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<210> 124  
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oligonucleotide 83

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aatactgaaa gtttttaag atatcatc 28

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oligonucleotide 84

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<210> 126  
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oligonucleotide 85

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<210> 127  
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<210> 128  
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tatacagaac cgattttatt taatccacc 29

<210> 129  
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<210> 130  
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<210> 132  
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<210> 133  
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<210> 136  
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<210> 137  
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<210> 138  
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oligonucleotide 97

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<210> 139  
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oligonucleotide 98

<400> 139  
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<210> 140

<211> 31  
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oligonucleotide 99

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<210> 143  
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<210> 144  
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oligonucleotide 103

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oligonucleotide 104

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gctaatgcag gaagtttacc tacttat 27

<210> 146  
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oligonucleotide 105

<400> 146  
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<210> 147  
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oligonucleotide 106

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<210> 148  
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oligonucleotide 107

<400> 148  
attaccattg tttaaaggcat ctgc 24

<210> 149  
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oligonucleotide 108

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<210> 150  
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oligonucleotide 109

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tcgggtacta cgttattaaa aggtccagg 29

<210> 151  
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oligonucleotide 110

<400> 151  
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oligonucleotide 111

<400> 152  
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<210> 153  
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oligonucleotide 112

<400> 153  
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<210> 154

<211> 35

<212> DNA

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<210> 155

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<223> Artificial sequence description:  
oligonucleotide 114

<400> 155  
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<210> 156

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<212> DNA

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<210> 157

<211> 32

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<210> 158  
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<220>  
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oligonucleotide 117

<400> 158  
gtggtgaata ttatataaaaa agaattgaaa tt 32

<210> 159  
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<220>  
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oligonucleotide 118

<400> 159  
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<210> 160  
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<212> DNA  
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<220>  
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oligonucleotide 119

<400> 160  
cgagaagcgg aagaggaatt agaagcggcg 30